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P#9

RAW SEQUENCE LISTING

DATE: 09/04/2002

PATENT APPLICATION: US/09/724,586

TIME: 11:57:34

Input Set : N:\Crf3\RULE60\09724586.raw

Output Set: N:\CRF4\09042002\I724586.raw

1 <110> APPLICANT: Sakowicz, Roman
 2 Goldstein, Lawrence S. B.
 3 The Regents of the University of California
 4 <120> TITLE OF INVENTION: Identification and Expression of a Novel Kinesin Motor
 5 Protein
 6 <130> FILE REFERENCE: 18557C-000710US
 7 <140> CURRENT APPLICATION NUMBER: 09/724,586
 8 <141> CURRENT FILING DATE: 2000-11-28
 10 <150> PRIOR APPLICATION NUMBER: US/09/235,416
 11 <151> PRIOR FILING DATE: 1999-01-22
 14 <150> PRIOR APPLICATION NUMBER: WO PCT/US99/01355
 15 <151> PRIOR FILING DATE: 1999-01-22
 16 <150> PRIOR APPLICATION NUMBER: US 60/072,361
 17 <151> PRIOR FILING DATE: 1998-01-23
 18 <160> NUMBER OF SEQ ID NOS: 7
 19 <170> SOFTWARE: PatentIn Ver. 2.0
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 784
 23 <212> TYPE: PRT
 24 <213> ORGANISM: Thermomyces lanuginosus
 25 <220> FEATURE:
 26 <223> OTHER INFORMATION: TL-gamma ATP-dependent plus end-directed
 27 microtubule motor protein
 28 <220> FEATURE:
 29 <221> NAME/KEY: DOMAIN
 30 <222> LOCATION: (1)..(357)
 31 <223> OTHER INFORMATION: kinesin-like microtubule motor domain
 32 <220> FEATURE:
 33 <221> NAME/KEY: DOMAIN
 34 <222> LOCATION: (358)..(442)
 35 <223> OTHER INFORMATION: neck domain links motor domain to stalk domain
 36 <220> FEATURE:
 37 <221> NAME/KEY: DOMAIN
 38 <222> LOCATION: (443)..(601)
 39 <223> OTHER INFORMATION: stalk domain, unc-104 family domain
 40 <220> FEATURE:
 41 <221> NAME/KEY: DOMAIN
 42 <222> LOCATION: (602)..(784)
 43 <223> OTHER INFORMATION: tail domain
 44 <400> SEQUENCE: 1
 45 Met Ser Gly Gly Gly Asn Ile Lys Val Val Val Arg Val Arg Pro Phe
 46 1 5 10 15
 47 Asn Ala Arg Glu Ile Asp Arg Gly Ala Lys Cys Ile Val Arg Met Glu

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48		20		25		30	
49	Gly	Asn	Gln	Thr	Ile	Leu	Thr
50		35		40		45	
51	Arg	Lys	Ser	Gly	Lys	Thr	Ile
52		50		55		60	
53	Asp	Arg	Ser	Tyr	Trp	Ser	Phe
54		65		70		75	
55	Gln	Glu	Asp	Leu	Phe	Gln	Asp
56				85		90	
57	Phe	Lys	Gly	Tyr	Asn	Asn	Cys
58				100		105	
59	Gly	Lys	Ser	Tyr	Ser	Met	Met
60				115		120	
61	Pro	Arg	Ile	Cys	Gln	Asp	Met
62				130		135	
63	Asp	Lys	Asn	Leu	Thr	Cys	Thr
64				145		150	
65	Asn	Glu	Arg	Val	Arg	Asp	Leu
66				165		170	
67	Lys	Val	Arg	Glu	His	Pro	Ser
68				180		185	
69	Lys	Leu	Val	Val	Arg	Ser	Phe
70				195		200	
71	Gly	Asn	Lys	Ala	Arg	Thr	Val
72				210		215	
73	Ser	Arg	Ser	His	Ala	Val	Phe
74				225		230	
75	Asp	Glu	Glu	Thr	Lys	Met	Asp
76				245		250	
77	Val	Asp	Leu	Ala	Gly	Ser	Glu
78				260		265	
79	Ala	Arg	Leu	Lys	Glu	Gly	Ala
80				275		280	
81	Gly	Arg	Val	Ile	Ala	Ala	Leu
82				290		295	
83	Lys	Asn	Gln	Leu	Val	Pro	Tyr
84				305		310	
85	Lys	Asp	Ser	Leu	Gly	Gly	Asn
86				325		330	
87	Ser	Pro	Ala	Asp	Ile	Asn	Phe
88				340		345	
89	Ala	Asp	Ser	Ala	Lys	Arg	Ile
90				355		360	
91	Pro	Asn	Ala	Arg	Met	Ile	Arg
92				370		375	
93	Arg	Ser	Lys	Leu	Gln	Ser	Gly
94				385		390	
95	Ser	Gly	Gly	Pro	Val	Glu	Glu
96				405		410	

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97      Lys Gln Ile Val Ser Ile Gln Gln Pro Asp Ala Thr Val Lys Lys Met
98              420              425              430
99      Ser Lys Ala Glu Ile Val Glu Gln Leu Asn Gln Ser Glu Lys Leu Tyr
100             435              440              445
101      Arg Asp Leu Asn Gln Thr Trp Glu Glu Lys Leu Ala Lys Thr Glu Glu
102             450              455              460
103      Ile His Lys Glu Arg Glu Ala Ala Leu Glu Glu Gly Ile Ser Ile
104             465              470              475              480
105      Glu Lys Gly Phe Val Gly Pro Tyr His Ser Lys Glu Met Pro His Leu
106              485              490              495
107      Val Asn Leu Ser Asp Asp Pro Leu Leu Ala Glu Cys Leu Val Tyr Asn
108              500              505              510
109      Ile Lys Pro Gly Gln Thr Arg Val Gly Asn Val Asn Gln Asp Thr Gln
110              515              520              525
111      Ala Glu Ile Arg Leu Asn Gly Ser Lys Ile Leu Lys Glu His Cys Thr
112              530              535              540
113      Phe Glu Asn Val Asp Asn Val Val Thr Ile Val Pro Asn Glu Lys Ala
114             545              550              555              560
115      Ala Val Met Val Asn Gly Val Arg Ile Asp Lys Pro Thr Arg Leu Arg
116              565              570              575
117      Ser Gly Tyr Arg Ile Ile Leu Gly Asp Phe His Ile Phe Arg Phe Asn
118              580              585              590
119      His Pro Glu Glu Ala Arg Ala Glu Arg Gln Glu Gln Ser Leu Leu Arg
120              595              600              605
121      His Ser Val Thr Asn Ser Gln Leu Gly Ser Pro Ala Pro Gly Arg His
122              610              615              620
123      Asp Arg Thr Leu Ser Lys Ala Gly Ser Asp Ala Asp Gly Asp Ser Arg
124             625              630              635              640
125      Ser Asp Ser Pro Leu Pro His Phe Arg Gly Lys Asp Ser Asp Trp Phe
126              645              650              655
127      Tyr Ala Arg Arg Glu Ala Ala Ser Ala Ile Leu Gly Leu Asp Gln Lys
128              660              665              670
129      Ile Ser His Leu Thr Asp Asp Glu Leu Asp Ala Leu Phe Asp Asp Val
130              675              680              685
131      Gln Lys Ala Arg Ala Val Arg Arg Gly Leu Val Glu Asp Asn Glu Asp
132             690              695              700
133      Ser Asp Ser Gln Ser Ser Phe Pro Val Arg Asp Lys Tyr Met Ser Asn
134             705              710              715              720
135      Gly Thr Ile Asp Asn Phe Ser Leu Asp Thr Ala Ile Thr Met Pro Gly
136              725              730              735
137      Thr Pro Arg Ser Asp Asp Asp Gly Asp Ala Leu Phe Phe Gly Asp Lys
138              740              745              750
139      Lys Ser Lys Gln Asp Ala Ser Asn Val Asp Val Glu Glu Leu Arg Gln
140             755              760              765
141      Gln Gln Ala Gln Met Glu Glu Ala Leu Lys Thr Ala Lys Gln Glu Phe
142             770              775              780
144 <210> SEQ ID NO: 2
145 <211> LENGTH: 2352
146 <212> TYPE: DNA

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147 <213> ORGANISM: Thermomyces lanuginosus
148 <220> FEATURE:
149 <223> OTHER INFORMATION: TL-gamma ATP-dependent plus end-directed
150 microtubule motor protein
151 <400> SEQUENCE: 2
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153 atcgaccgtg gcgcaaaatg tattgtgcgg atggaaggaa atcaaaccat cctcaccctt 120
154 cctccgggtg ccgaagagaa ggcgcgtaaa agtggcaaaa ctattatgga tggcccgaag 180
155 gcatttgctg tcgatcggtc gtattggtcc ttgacaaga atgctcccaa ctatgegaga 240
156 caggaagacc tattccaaga tctcggagtc ccgcttctgg ataatgcatt caagggttat 300
157 aacaattgta tcttcgccta cggtcagacc gggtcgggca agtcctattc aatgatgggc 360
158 tatggcaagg agcatggcgt gatcccgctg atttgccagg acatgttccg gcgtattaat 420
159 gaactgcaga aggacaagaa cctcacttgc accgtcgaag tttcgtactt ggaaatttac 480
160 aatgaacgag tgcgagactt gctgaatccg tcgacaaagg ggaatctcaa ggtccgagaa 540
161 caccgcgtga ccggccccta cgtggaggac ttggcgaagc tggctcgtgc atcattccaa 600
162 gaaatcgaaa atctcatgga tgagggcaac aaagccagaa cggttgcgcg cacaacatg 660
163 aacgagacat ccagtcgatc ccacgcgcgt ttcactttga ccttgacgca aaagtggcat 720
164 gatgaagaga ccaaaatgga cacagagaag gttgcgaaga tcagtctggt agatttggcg 780
165 ggttctgagc gagcaacgtc caccggagct actggagcgc gactgaagga ggggtgcagag 840
166 atcaaccgct cactttcgac cctaggctgt gtgattgcag cgctagcggg tatgtcgtcg 900
167 ggaaaacaga agaagaatca gttagtacct taccgagatt cggtagtgac gtggcttctg 960
168 aaggactcct tgggaggcaa ctcgatgacc gccatgattg ccgccatttc gcctgctgat 1020
169 attaaactttg aagagactct cagtaccctt cgaatagcgg actctgcgaa gcgaatcaag 1080
170 aaccacgcag tggatcaatga agaccggaac gcgcggatga tccgcgagtt gaaggaggaa 1140
171 ctgcgcgagc tgaggagcaa actccagagc agtgggtggg gtggagggtg tgcaaggagg 1200
172 tctggcgggc cagtggagga atcgtaaccg ccgacacgc cgctcgagaa gcaaatcggt 1260
173 tcgattcagc agccggatgc gacagtcaag aaaatgagca aggcagaaat cgtggagcaa 1320
174 ctgaaccaga gtgagaagct ctatcgggat ctcaatcaga cctgggaaga gaagctggcc 1380
175 aagaccgagg aaatccacaa ggaacgagaa gcggcgctcg aggagctggg tatcagcatc 1440
176 gaaaagggct ttgttggtcc ttaccactcc aaagaaatgc cacatctagt caacttgagc 1500
177 gatgactctc ttctggctga gtgtcttgtc tacaacatca agcccgggca gacaagggtt 1560
178 ggaaacgtca accaagatac acaagcggaa attcgtctga acggttcgaa gatcctgaaa 1620
179 gaacactgta cgtttgaaaa tgtggacaac gttgtgacca tcgtgccaaa cgagaaggct 1680
180 gctgtcatgg tgaacggcgt gcgaatcgac aagcctactc gcctccgcag cggctacagg 1740
181 atcatcctgg gcgatttcca catttttoga ttcaaccatc cggaagaagc tcgtgcggaa 1800
182 cggcaagaac aatccttgct tcgccattct gtcaccaaca gtcagttggg ttgcctgctc 1860
183 ccaggccgtc acgaccggac actgagcaag gcgggttcgg atgcggacgg cgattctcgc 1920
184 tcagattctc ctttgccgca ctttcgtgga aaggatagcg actggttcta tgctcgcagg 1980
185 gaagctgcta gcgcgatcct agggttggat cagaagatct ctcatctgac agatgacgag 2040
186 ttgatgcat tatttgacga tgttcagaaa gcgcgggcag ttctgctgtg gctggtcgaa 2100
187 gacaacgaag atagcgattc gcagagttcg tttccggtcc gtgacaaata catgtccaat 2160
188 ggaaccattg ataatttctc gctcgatacc gccattacta tgccgggtac ccctcgtagt 2220
189 gatgacgagc gtgacgcgct gttttttggt gataagaagt cgaaacagga tgcgtctaata 2280
190 gttgatgttg aggagttgcy tcaacagcag gctcagatgg aagaagccct gaaaacagcg 2340
191 aagcaggaat tc 2352
193 <210> SEQ ID NO: 3
194 <211> LENGTH: 21
195 <212> TYPE: DNA
196 <213> ORGANISM: Artificial Sequence

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197 <220> FEATURE:
198 <223> OTHER INFORMATION: Description of Artificial Sequence:primer
199 <400> SEQUENCE: 3
200     atgtcgggcg gtggaaatat c                               21
202 <210> SEQ ID NO: 4
203 <211> LENGTH: 23
204 <212> TYPE: DNA
205 <213> ORGANISM: Artificial Sequence
206 <220> FEATURE:
207 <223> OTHER INFORMATION: Description of Artificial Sequence:primer
208 <400> SEQUENCE: 4
209     gaattcctgc ttcgctgttt tca                               23
211 <210> SEQ ID NO: 5
212 <211> LENGTH: 30
213 <212> TYPE: DNA
214 <213> ORGANISM: Artificial Sequence
215 <220> FEATURE:
216 <223> OTHER INFORMATION: Description of Artificial Sequence:degenerate
217     forward primer
218 <220> FEATURE:
219 <221> NAME/KEY: modified_base
220 <222> LOCATION: (25)
221 <223> OTHER INFORMATION: n = a, c, g or t
222 <400> SEQUENCE: 5
W--> 223     gcgcggatcc atytttygcht ayggncarac                     30
225 <210> SEQ ID NO: 6
226 <211> LENGTH: 30
227 <212> TYPE: DNA
228 <213> ORGANISM: Artificial Sequence
229 <220> FEATURE:
230 <223> OTHER INFORMATION: Description of Artificial Sequence:degenerate
231     reverse primer
232 <220> FEATURE:
233 <221> NAME/KEY: modified_base
234 <222> LOCATION: (16)
235 <223> OTHER INFORMATION: n = a, c, g or t
236 <220> FEATURE:
237 <221> NAME/KEY: modified_base
238 <222> LOCATION: (28)
239 <223> OTHER INFORMATION: n = a, c, g or t
240 <400> SEQUENCE: 6
W--> 241     gcgcgaattc tcdganccdg cvarrtcnac                     30
243 <210> SEQ ID NO: 7
244 <211> LENGTH: 30
245 <212> TYPE: DNA
246 <213> ORGANISM: Artificial Sequence
247 <220> FEATURE:
248 <223> OTHER INFORMATION: Description of Artificial Sequence:degenerate
249     reverse primer

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 09/04/2002
PATENT APPLICATION: US/09/724,586 TIME: 11:57:36

Input Set : N:\Crf3\RULE60\09724586.raw
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; N Pos. 25
Seq#:6; N Pos. 16,28
Seq#:7; N Pos. 16,28

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 4

VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\09724586.raw

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L:223 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
L:241 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
L:259 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0